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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
- (F) ZIP: 92037
- (G) TELEPHONE: (619) 784-2937
- (H) TELEFAX: (619) 784-9399

(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACTTCCA TGAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCCTCCGC CAATCAGTCG	180
TAAAACAGAA GTCGTGGAAA GCGGATAGAA AGAATGTTCG ATTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCCG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTTCTGTC CAGATCGAAC TCAAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTCATGTTA GTTTCGGCT	420
GAGCAACAAT TAAAGTTATG TTTCAGTTCC GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTTAGAACAA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTT	540
TTTTAATGAT AAGCATTTCG TCGTTTATAC TTTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTGATTT TAATCGCCAG ATAAGCAATA TATTGTGTAATATTTGTAT TCTTTATCAG	660
GAAATTCAAG GAGACGGGAG AGTTACTATC TACTAAAAGC CAAACAATTT CTTACAGTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCCG ATGTGACTAG CTCTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCCATGC CCCATGTGCC CCACCAAGAG	180
TTTGCATCC CATAAAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC	240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT	300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTCCAA AATGTATAAA ACCGAGAGCA	360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA	420
CTAAAGG	427

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGTTGCAGG ACAGGGATGTG GTGCCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCCAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACGG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCGGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAGCAGC AAAATCAAGT GAATCATCTC AGTGAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTGAT GGTGATGAGT TGTCTATGT GGACTTGGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCCTGAG TTTGGCCAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACAACTTGG GAATCTTGAC TAAGAGGTCA AATTCACCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTTCCCCAA GTCCCTGTG CTGCTGGTC	840
AGCCCAACAC CCTTATCTGC TTTGTGGACA ACATCTCCC ACCTGTGATC AACATCACAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGAGC GCGTTTATGA GACCAGCTTC CTCGTCAACC	960
GTGACCATTG CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCCTCTGAT GATGACATT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGGT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAACGTGGT GTGTGCCCTG GGGTTGTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAAACTTT CCATGAAAAA TATGGAAAAA TATATGAAAA TTGAGAAATC CAAAAAAACTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAAGTTCCTC CGCCAATCAG TCGTAAAACA GAAGTCGTGG AAAGCGGATA GAAAGAATGT	1560
TCGATTTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAATATAG CGGTGAGTGA GCGGGAAGCT CGGTTCTGT	1680
CCAGATCGAA CTCAAAACCA GTCCAGCCAG TCGCTGTGAA AACTAATTAA GTAAATGAGT	1740

TTTCATGTT AGTTCGCC TGAGCAACAA TIAAGTTAT GTTCAGTTC GGCTTAGATT	1800
TCGCTGAAGG ACTTGCAC TTCAATCAAT ACCTTACAAC AAAATCAAAA CTCATTCTAA	1860
TAGCTTGGTG TTCATCTTT TTTTAATGA TAAGCATTG TCGTTATA CTTTTATAT	1920
TTCGATATTA AACCACCTAT GAAGTCATT TTAATGCCA GATAAGGAAT ATATTGTGA	1980
AATATTGTG TTCTTATCA GGAAATTCAG GGAGACGGGG AAGTTACTAT CTACTAAAAG	2040
CCAAACAATT TCTTACAGTT TTACTCTCTC TACTCTAGAG CTTGGCACTG GCCGTCGTT	2100
TACAACGTCG TGACTGGAA AACCCCTGGCG TTACCCAACT TAATGCCCT GCAGCACATC	2160
CCCCTTCGC CAGCTGGCGT AATAGCGAAG AGGCCGCAC CGATGCCCT TCCCAACAGT	2220
TGGCAGCCT GAATGGCGAA TGGCGCCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG	2280
GTATTCACA CCGCATATGG TGCCTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA	2340
GCCAGCCCCG ACACCCGCCA ACACCCGCTG ACCGCCCTG ACGGGCTTGT CTGCTCCGG	2400
CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG AGGTTTCAC	2460
CGTCATCACC GAAACCGCG AGACGAAAGG GCCTCGTAC ACCCTATT TTATAGGTTA	2520
ATGTCTGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTGGGAA AATGTGGCG	2580
GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT	2640
AACCCGTATA AATGCTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTCC	2700
GTGTCGCCCT TATTCCCTT TTTGCGGCAT TTTGCCCTCC TGTTTTGCT CACCCAGAAA	2760
CGCTGGTGAAG AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACCAGTGGGT TACATGAAAC	2820
TGGATCTCAA CAGCGTAAG ATCCCTGAGA GTTTGCCCG CGAAGAACGT TTTCAATGA	2880
TGAGCACTTT TAAAGTTCTG CTATGTGGG CGGTATTATC CCGTATTGAC GCCGGGCAAG	2940
AGCAACTCGG TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAAGTCA	3000
CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA	3060
TGAGTGATAA CACTGGGCC AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA	3120
CCGCTTTTT GCACAACATG GGGGATCATG TAACTGCCCT TGATCGTTGG GAACCGGAGC	3180
TGAATGAAGC CATAACAAAC GACCGAGCGTG ACACCAACGAT GCCTGTAGCA ATGGCAACAA	3240
CGTTGCGCAA ACTATTAACG GCGGAACATAC TTACTCTAGC TTCCCGGCAA CAATTAATAG	3300
ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTCTGCG CTGGCCCTT CCGGCTGGCT	3360
GGTTTATTGC TGATAAAATCT GGAGCCGGTG AGCGTGGTC TCGGGTATC ATTGCAGCAC	3420
TGGGCCAGA TGGTAAGCCC TCCCCTATCG TAGTTATCTA CACGACGGGG AGTCAGGCAA	3480
CTATGGATGA ACGAAATAGA CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGT	3540
AACTGTAGA CCAAGTTAC TCATATATAC TTTAGATTGA TTIAAAACTT CATTNTTAAT	3600
TTAAAAGGAT CTAGGTGAAG ATCCTTTTG ATAATCTCAT GACCAAAATC CCTTAAGGTG	3660
AGTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT TCTTGAGATC	3720
CTTTTTCT CGCGTAATC TGCTGCTTGC AAACAAAAAA ACCACCGCTA CCAGCGGTGG	3780
TTTGTGCGGC GGATCAAGAG CTACCAACTC TTTTCCGAA GGTAACTGGC TTCAGCAGAG	3840
CCGAGATACC AAATACTGTC CTTCTAGTGT AGCCGTAGTT AGGCCACCCAC TTCAAGAACT	3900
CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG	3960
GCGATAAGTC GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACGGAT AAGGCGCAGC	4020
GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT GGAGCGAACG ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCAGA GGGAGAAAGG	4140
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA CGGCACGAGG GAGCTTCAG	4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	4260
GATTTTGTC ATGCTCGTCA GGGGGCCGG A GCCTATGGAA AAACGCCAGC AACGGCCCT	4320
TTTTACGGTT CCTGGCCTT TGCTGGCCTT TTGCTCACAT GTTCTTCCT GCGTTATCCC	4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	4440
GAACGACCGA CGCGAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGGCCCA ATACGCAAAC	4500
CGCCTCTCCC CGCGCGTTGG CGGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT	4560
GGAAAGCGGG CAGTGAGCGC AACGCAATT AATGTGAGTTA GCTCACTCAT TAGGCACCCC	4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAAT	4680
TTCACACAGG AAACAGCTAT GACCATGATT ACG	4713

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTTGCAGG ACAGGATGTG GTGCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCGA CGGCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGGCC ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCCGGCCG CGGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGGG TTTCCAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAAGCAG AAAATCAAGT GAATCATCTC AGTGCACACTA	420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC	480
TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCAG GGACTGAGGG CGGAAACTCC	540
GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC	600
ATACGGCTCG TGACCAAGATA CATCTACAAAC CGGGAGGAGT ACGTGCCTA CGACAGCGAC	660
GTGGCGAGT ACCGGCGGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC	720

CAGCCGGAGA TCCTGGAGCG AACGCCGCC GAGGTGGACA CGCGTGCAG ACACAAC	780
GAGGGGCCGG AGACCAGCAC CTCCCTGCGG CGGCTTGAAC AGCCCAATAT CGCCATCTCC	840
CTGTCCAGGA CAGAGGCCCT CAACCACCAC AACACTCTGG TCTGTTCGGT GACAGATTTC	900
TACCCAGCCA AGATCAAAGT GCGCTGGTTC AGGAATGGCC AGCAGGAGAC AGTGGGGTC	960
TCATCCACAC AGCTTATTAG GAATGGGCAC TGGACCTTCC AGGTCTGCGT CATGCTGGAG	1020
ATGACCCCTC ATCAGGGAGA GGTCTACACC TGCCATGTGG AGCATCCCAG CCTGAAGAGC	1080
CCCATCACTG TGGAGTGGAG GCCACAGTCC GAGTCTGCCG GGAGCAAGAT GTTGAGCGGC	1140
ATCGGGGGCT GCGTGCTTGG GGTGATCTTC CTCGGGCTCG GCCTTTCAT CCGTCACAGG	1200
AGTCAGAAAG GACCTCGAGG CCCTCCTCCA GCAGGGCTCC TGCAAGTGCAGT CAGAGTGT	1260
TGACTCAGTT GACTGTCTCA GACTGTAAGA CCTACATGTC TCGAATTGCA GCTCGGTACC	1320
CGGGGATCCT CTAGAGTCGA CCTGCAGGCA TGCAATTGCA TGCAACTCTCA CATTCTCTC	1380
CTAATACGAT AATAAAACTT TCCATGAAAA ATATGAAAA ATATATGAAA ATTGAGAAAT	1440
CCAAAAAAACT GATAAACGCT CTACTTAATT AAAATAGATA AATGGGAGCG GCAGGAATGG	1500
CGGAGCATGG CCAAGTTCCT CCGCCAATCA GTCGTAAAC AGAAAGTCGTG GAAAGCGGAT	1560
AGAAAGAATG TTGATTGCA CGGGCAAGCA TGTCTGCTAT GTGGCGGATT CGGGAGGAAT	1620
TGCACTGGAG ACCAGCAAGG TTCTCATGAC CAAGAATATA GCGGTGAGTC AGCGGGAAAGC	1680
TCGGTTTCTG TCCAGATGCA ACTCAAAACT AGTCCAGCCA GTCGCTGTG AAACATAATTA	1740
AGTAAATGAG TTTTCATGT TAGTTCGCG CTGAGCAACA ATTAAGTTA TGTTTCAGTT	1800
CGGCTTAGAT TTGCTGAAG GACTGCCAC TTTCAATCAA TACTTTAGAA CAAAATCAA	1860
ACTCATTCTA ATAGCTTGGT GTTCATCTTT TTTTTAATG ATAAGCATT TGTCGTTTAT	1920
ACTTTTTATA TTTCGATAATT AAACCACCTA TGAAGTTCAT TTTAATGCC AGATAAGCAA	1980
TATATTGTGT AAATATTGT ATTCTTTATC AGGAAATTCA GGGAGACGGG GAAGTTACTA	2040
TCTACTAAAA GCCAAACAAT TTCTTACAGT TTTACTCTCT CTACTCTAGA GCTTGGCACT	2100
GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCCTGGC GTTACCCAAC TTAATGCCCT	2160
TGCAGCACAT CCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATGCC	2220
TTCCCAACAG TTGCCAGGCC TGAATGGCGA ATGGCCCTG ATGCCGTATT TTCTCCTTAC	2280
GCATCTGTGC GGTATTTCAC ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC	2340
CGCATAGTTA AGCCAGCCCC GACACCCGCC AACACCCGCT GACGCCCT GACGGGCTG	2400
TCTGCTCCCC GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA	2460
GAGGTTTCA CCGTCATCAC CGAAACGCCG GAGACGAAAG GGCCTCGTGA TACGCCATT	2520
TTTATAGGTT AATGTATGCA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTCCGGG	2580
AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT	2640
CATGAGACAA TAACCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT	2700
TCAACATTTC CGTGTGCCCT TTATTCCCTT TTTGGGCA TTTGCCCTC CTGTTTTGC	2760
TCACCCAGAA ACGCTGGTGA AAGTAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGG	2820
TTACATCGAA CTGGATCTCA ACAGCCGTAAC GATCCTTGAG AGTTTCCGCC CCGAAGAACG	2880
TTTCTCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTATTGA	2940
CGCCGGGCAA GAGCAACTCG GTCGCCGCAT ACACATTCT CAGAATGACT TGGTTGAGTA	3000
CTCACCCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAAT TATGCAGTGC	3060

TGCCATAACC ATGAGTGATA ACACGTGGC CAACTTACTT CTGACAACGA TCGGAGGACC	3120
GAAGGAGCTA ACCGCTTTT TGCACAACAT GGGGGATCAT GTAACCGCC TTGATCGTTG	3180
GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC	3240
AATGGCAACA ACGTTGCGCA AACTATTAAAC TGGCGAACTA CTTACTCTAG CTTCCGGCA	3300
ACAATTAAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACCTCTGC GCTCGGCCCT	3360
TCCGGCTGGC TGGTTTATTG CTGATAAAATC TGGAGCCGGT GACCGTGGGT CTCGGGTAT	3420
CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG	3480
GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT	3540
TAAGCATTGG TAACTGTCAG ACCAAGTTA CTCATATATA CTTTAGATTG ATTAAAATC	3600
TCATTTTAA TTTAAAAGGA TCTAGGTGAA GATCCTTTT GATAATCTCA TGACCAAAAT	3660
CCCTTAACGT GAGTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC	3720
TTCTTGAGAT CCTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCAACCGCT	3780
ACCAGCGGTG GTTTGTTGC CGGATCAAGA GCTACCAACT CTTTTCCGA AGGTAACCTGG	3840
CTTCAGCAGA GCGCAGATAAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA	3900
CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCACTGGC	3960
TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA	4020
TAAGGCGCAG CGGTGGGCT GAACGGGGGG TTCGTGCACA CAGCCAGCT TGGAGCGAAC	4080
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCGA	4140
AGGGAGAAAG GCGGACAGGT ATCCGTAAG CGGCAGGGTC GGAACAGGAG AGGGCACCGAG	4200
GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTGGGTTTC GCCACCTCTG	4260
ACTTGAGCGT CGATTTTGT GATGCTCGTC AGGGGGCGG AGCTATGGA AAAACGCCAG	4320
CAACCGGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTCC	4380
TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTGAGTGAG CTGATAACCGC	4440
TCGCCGCAGC CGAACGACCG AGCCGAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC	4500
AATACGCAAAC CGGCCTCTCC CGCGCGTTG GCGGATTCTAT TAATGCAGCT GGCACGACAG	4560
GTTCGGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT AGCTCACTCA	4620
TTAGGCACCC CAGGCTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG	4680
CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACG	4724

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGG A GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTGGGATCCT CAGCTCAGGA ATCCTCTTG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGGATCCT CACAAGGGCC CTTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

100

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGCC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCG

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCTTGCAGG ACAGGATGTG GTGCCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCCA CGGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCG ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCCCCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACCGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCCATAC TGGCAACCG CCCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTGTT CTGTCCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCCGAAATCT GCCAAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCCGTCC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGACC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAACTG GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTGTT GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGCCCTG GGAGTGACCA GCCAGGAAC	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACTTTCCA	1200
TGAAAAATAT GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCCCTCCG	1320
CAATCAGTCG TAAAACAGAA GTCGTGGAAA GCGGATAGAA AGAATGTTCG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAAACTAGTC CAGCCAGTCG CTGTCGAAAC TAATTAAGTA AATGAGTTTT TCATGTTAGT	1560
TTCCGCGCTGA GCAACAATTA AGTTTATGTT TCAGTTGGC TTAGATTTCG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAAACTC ATTCTAATAG CTTGGTGTTC	1680
ATCTTTTTT TTAATGATAA GCATTTGTC GTTTATACCTT TTTATATTC GATATTAAAC	1740
CACCTATGAA GTTCATTITA ATGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATTC	1800
TTTATCAGGA AATTCAAGGAA GACGGGGAAAG TTACTATCTA CTAAAAGCCA AACAAATTCT	1860
TACAGTTTA CTCTCTCTAC TCTAGAGCTT GGCACTGGCC GTCGTTTAC AACGTCGTGA	1920
CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTCT CCTTACGGAT CTGTGCGGTA TTTCACACCG	2100

CATATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA	2160
CCCGCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG	2220
ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA	2280
ACGCCGGAGA CGAAAGGGCC TCGTGATACG CCTATTGTTA TAGGTTAACAT TCATGATAAT	2340
AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTG	2400
TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAAT	2460
GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCTGT TCGCCCTTAT	2520
TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT	2580

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGGGCGACC TT 32

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTGACCC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCGG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGGATCCC TATGGCCGGA AGGCCTG

27

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCCT GTCAGAACATGG CCACCAT

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTATATA CAGCACATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATT ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATAACAG GGCGTACACT TTCCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTG ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCCG GGTTAAAAAC ATGTATCACT TTTGTCGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTCTG GTACCATGCC GGAGGAGGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met
1 5 10